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## Introduction to the Allen Institute Single Cell Ecosystem

*Monday 9 September 2024 10:30 (1h 30m)*

The Allen Institute for Brain Science (in collaboration with BICCN/BICAN) has recently created multiple large-scale transcriptomic taxonomies from single cell (sc)- and single nucleus (sn)-RNA sequencing, covering various species and disease states. To increase the usage and understanding of these taxonomies beyond their publications, the Institute created multiple web-based interactive tools. These tools allow neuroscience researchers to freely sort through, visualize, and analyze different taxonomy datasets directly from their browser. The first tool featured in this presentation is the Allen Brain Cell (ABC) Atlas, which is an interactive brain cell atlas featuring sc/snRNA-seq cell type taxonomies of: the whole mouse brain (Yao et al., 2023, Zhang et al., 2023), the whole human brain (Siletti et al., 2023), and two cortical regions (MTG and DLPFC) from brains with Alzheimer's disease (Gabbito and Travaglini et al., 2024). Both the whole mouse brain and the MTG/DLPFC Alzheimer's taxonomies feature spatial transcriptomic MERFISH data as well. The second tool featured is MapMyCells, which is a tool for mapping transcriptomic data onto the cell type taxonomies previously listed in the ABC Atlas. The third tool is the Cell Type Knowledge Explorer, which features: sc/snRNA-seq cell type taxonomies of the primary motor cortex of mouse, human, and marmoset (BICCN 2021); accompanying mouse patch-seq data showing electrophysiological and morphological characteristics (Scala et al., 2021), and an integrated mouse-human-marmoset taxonomy to identify cross-species cell type homologies (Bakken et al., 2021). All three tools will be demonstrated live with example use cases to introduce users how to use these tools for their own research questions and hypothesis testing. Users will need internet access, no prior software downloads are needed

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**Session Classification:** Hands-on Session 1